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PRISUL-1
AAB82038
ID: AAB82038 standard, peptide, 12 AA.
XX
AAB82038;
XX
15-JUN-2001 (first entry)
XX
XX Human, hepatocyte, cytosate; anti-HIV; antibiotic;
FW Human, hepatocyte, cytosate; anti-HIV; antibiotic;

No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES						
Result No.	Score	Query Match	Length	DB ID	Description	FTS
1	60	100.0	12	22	AAHE2038 Human hepatocyte	XX
2	60	100.0	13	22	AAHB2037 Human hepatocyte	PN
3	60	100.0	34	22	AAHB2020 Human hepatocyte	XX
4	60	100.0	436	22	AGG73954 Human colon cancer	PD
5	60	100.0	586	20	ARY27443 Amino acid sequence	17-MAR-2001
6	63	109.0	622	22	AAU303001 Novel human secret	XX
7	60	100.0	635	21	AAE53356 Human colon cancer	PA
8	55	91.7	11	22	AAHB2039 Human hepatocyte	XX
9	52	86.7	52	22	AAU033060 Novel human secret	P1
10	41	68.3	27	20	AAV27444 Antennozinc inter	WPT

Novel regulatory or unfolding peptides of ezrin that binds to hepreceptor, useful for inducing immune response for treating infectious diseases and cancer.

HIV-related dementia. The present peptide binds to domain A of the heparceptor (AA82019).

AC AAC7443; ! XX !
 RESULT 4
 AAC7443
 ID AAC7443 standard; protein, 436 AA.
 XX
 AC AAC7454;
 XX
 ID AAC7454 standard; protein, 436 AA.
 XX
 DR 03-SEP-2091 (first entry)
 XX
 Human colon cancer antigen protein SEQ ID NO:4718.
 XX
 human; colon cancer; colon; cancer; antigen; diabetics; deterioration;
 colrectal carcinoma.
 XX
 Homo sapiens.
 OS
 PN WO200122950-A2;
 XX
 PD 23-SEP-1999.
 XX
 PR 18-MAR-1999; 99WO-EP-02054.
 XX
 PR 18-MAR-1998; 98US-0040725.
 XX
 PA (CHIBI-) INST CURIE,
 PA (CNRS) CNRS CENT NAT RECH SCI.
 XX
 Arpin M, Crepaldi T, Gautreau A, Louvard D;
 XX
 WPI: 1999-561851/47.
 XX
 New composition for prevention and treatment of tumors and metastasis
 PT -
 FS Example 1; Fig 1; 31pp; English.
 XX
 The invention provides a pharmaceutical composition containing ezrin
 protein, RNA or DNA mutated on tyrosine 353, or a functional fragment
 or derivative of the ezrin mutant, the new composition is useful for
 prevention and/or treatment of tumors, and especially metastasis. The
 present sequence represents the amino acid sequence of human ezrin,
 (hereinafter the nomenclature by deletion of the first amino acid Met).
 XX
 Sequence 586 AA;
 QC Query Match 100.0%; Score 507; Obj 29; Length 586;
 Best Local Similarity 100.0%; Pred. No. 0/12;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QC Query 1 EELMLRLQYEE 12
 Db 345 EELMLRLQYEE 356
 RESULT 6
 AAU3004
 AAU3004 standard; protein, 622 AA.
 XX
 AC AAU3004;
 XX
 Query Match 100.0%; Score 60; Obj 22; Length 436;
 Best Local Similarity 100.0%; Pred. No. 0/88;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 Sequence 436 AA;
 QC Query Match 100.0%; Score 60; Obj 22; Length 436;
 Best Local Similarity 100.0%; Pred. No. 0/88;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 AC AAU3004;
 XX
 LT 18 DEC 2001 (first entry)
 XX
 Novel human secreted protein #495.
 XX
 Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia;
 XX
 OS Homo sapiens.
 XX
 PN WO200179449-A2.
 XX
 PD 25-OCT-2001.

XX	(HUMA-) HUMAN GENOME SCI INC.
PF	16 · APR · 2001; 2001W0-US08656.
XX	
PF	18 · AUR · 2000; 2000US 0562929.
XX	
DE	26 · JAN · 2001; 2001US · 0770160.
XX	
PA	(HYSE-) HYSEQ INC.
XX	
PT	Jianq YI, Liu C, Drmanac RY;
XX	
DE	W01 · 2001 6117257/0.
XX	
PT	Nucleic acids encoding a family of human polypeptides, useful in genetic variation, testing and therapy
XX	
PS	Claim 20; Page 219; 765pp; English.
XX	
CC	The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptides. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haemopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukemias. AU19510-AAU3304 represent the amino acid sequences of novel human secreted proteins of the invention.
XX	
SQ	Sequence 622 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	622 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	622 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	622 AA.
XX	
RESULT	7
11:	AAB53356 Standard, Protein, 693 AA.
XX	
AC	AAB53356;
XX	
DE	09 · MAR · 2001 (first entry)
XX	
DE	Human colon cancer antigen protein sequence SEQ ID NO:896.
XX	
KW	Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW	identification; cytostatic; cardiotropic; neuroprotective; vulcanary;
KW	immunomodulatory; muscular; gravitational; gastrontestinal;
KW	neurotropic; anti-infective; antibacterial; gene therapy; wound;
KW	neural disorder; immune system disorder; muscular disorder;
KW	reproductive disorder; gastrointestinal disorder; renal disorder;
KW	infectious disease; cardiovascular disorder.
XX	
OS	Homo sapiens.
XX	
FN	W0200005451 A1.
XX	
FN	21 · SEP · 2000.
XX	
DE	08 · MAR · 2000; 2000W0-US05884.
XX	
DE	12 · MAR · 1999; 9405 0124279.
XX	
FN	17 · SEP · 1999; 99GB · 0021681.
XX	
PR	17 · SEP · 1999; 99GB · 0021881.
XX	
PA	(HOLM) HOLMS R D.
XX	
PI	Holms R D.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	
PT	Rosen CA, Ruben SM;
XX	
DR	WPI; 2000-59734/55.
XX	
DR	N PDB; AAC98113.
XX	
PT	Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon disorders such as colon cancer.
XX	
PS	Claim 11; Page 144-1451; 2104pp; English.
XX	
CC	AAC97991 to AAC98763 encode the human colon cancer-associated proteins, called human colon cancer antigens, given in AAB53234 to AAB54006. The human protective, immunomodulatory, dynaein, cardiotropic, muscular, pulmonary, nephrotopic, anti-infective and antibacterial activities, and neurotrophic, immunomodulatory, cytostatic, vulcanary, gravitational, gravitational, anti-infective and antibacterial activities, and can be used in gene therapy. The colon cancer antigen poly nucleotides, proteins and antibodies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The poly nucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent diseases such as neural disorders, immune system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders, wound, renal disorders, infectious diseases, and cardiovascular disorders. AAC98764 to AAC98772 and AAB54007 represent sequences used in the exemplification of the present invention.
XX	
SQ	Sequence 635 AA.
XX	
Query Match	100.0%
Best Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Best Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Best Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
RESULT	8
11:	AAB82039
XX	
DE	Human hepreceptor domain A binding peptide Rape2232.
XX	
KW	Human; hepreceptor; cytostatic; anti-HIV; antibiotic;
KW	neurotropic; immune response inducer; ezrin; infectious diseases; cancer; HIV-related dementia.
XX	
OS	Homo sapiens.
XX	
FT	location/qualifiers
XX	
FT	Key Modified-site
XX	
FT	note - "optionally phosphorylated"
XX	
IN	GR2354241-A.
XX	
FD	21 · MAR · 2001.
XX	
FF	17 · SEP · 1999; 99GB · 0021681.
XX	
PR	17 · SEP · 1999; 99GB · 0021881.
XX	
PA	(HOLM) HOLMS R D.
XX	
PI	Holms R D.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	
PT	Rosen CA, Ruben SM;
XX	
DR	WPI; 2000-59734/55.
XX	
PT	Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon disorders such as colon cancer.
XX	
PS	Claim 11; Page 144-1451; 2104pp; English.
XX	
CC	AAC97991 to AAC98763 encode the human colon cancer antigens, given in AAB53234 to AAB54006. The human protective, immunomodulatory, dynaein, cardiotropic, muscular, pulmonary, nephrotopic, anti-infective and antibacterial activities, and can be used in gene therapy. The colon cancer antigen poly nucleotides, proteins and antibodies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The poly nucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent diseases such as neural disorders, immune system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders, wound, renal disorders, infectious diseases, and cardiovascular disorders. AAC98764 to AAC98772 and AAB54007 represent sequences used in the exemplification of the present invention.
XX	
SQ	Sequence 635 AA.
XX	
Query Match	100.0%
Best Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELMLRLQYEE 392
Sequence	635 AA.
XX	
Query Match	100.0%
Host Local Similarity	100.0%
Matches	12;
QY	1 EELMLRLQYEE 12
19:	481 EELML

XX WPI: 2001-297207/31
 DR
 XX Novel regulatory peptide of ezrin that binds to
 PT receptor, useful for inducing immune response for treating
 PR infectious diseases and cancer
 XX Claim 26, Page 37, 47ff, Fig.11, st.
 XX
 CC The hepreceptor is a novel active site in human ezrin. Ezrin regulates
 CC the structure of the cortical cytoskeleton to control cell surface
 CC topography. The present invention relates to peptides (see AAB8221 to
 CC AAB82041) that bind to hepreceptor with greater affinity than HER1 (see
 CC AAB82046). The hepreceptor binding peptides are useful for inducing
 CC immune response, and for treating infectious diseases, cancer and
 CC HIV-related dementia. The present peptide binds to domain A of the
 CC hepreceptor (AAB8221c).
 XX Sequence 11 AA:
 CC
 Query Match 91.7%; Score 55; DB 22; Length 11;
 Rest local Similarity 100%; pred. No. 0.014;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 SQ
 ID AAB3060 standard; peptide: 52 AA.
 QY 2 ELMRLQDYE 12
 DB 1 ELMRLQDYE 11
 XX
 RESULT 9
 AAB3060 standard; peptide: 52 AA.
 ID AAB3060 standard; peptide: 52 AA.
 XX
 DT 18-DEC-2001 (first entry)
 DE Novel human secreted protein # 3551.
 XX
 KW Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; hematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200179449-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 16-APR-2001; 2001WO-US08656.
 XX
 PR 18-APR-2000; 2000US-0552929.
 PR 26-JAN-2001; 2001US-0770160.
 XX
 PA (HYSE-) HYSE INC.
 PR Tang YI, Liu C, Ormanac RT;
 XX
 DR WPI: 2001-611725/70.
 XX
 PT Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy.
 XX
 PS Claim 29; Page 792; 755pp; English.
 XX
 The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are used to
 CC determine the presence of or predisposition to a disease associated
 CC with altered levels of polypeptides. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising

CC the nucleic acids encoding the polypeptides and cells genetically
 CC engineered to express them are also useful for producing the proteins.
 CC The proteins are useful in genetic vaccination, testing and
 CC therapy, and can be used as nutritional supplements. They may be used to
 CC increase stem cell proliferation; to regulate hematopoiesis; and in
 CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
 CC immune suppression and/or stimulation; as anti-inflammatory agents; and
 CC as treatment of diseases. Amino acid sequence 354 represents the amino acid
 CC sequences of novel human secreted proteins of the invention.
 XX
 SQ Sequence 52 AA:
 CC
 Query Match 86.7%; Score 52; DB 22; Length 11;
 Rest Local Similarity 91.7%; pred. No. 9.2;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ELMRLQDYE 12
 DB 13 ELMRLQDYE 24
 XX
 RESULT 10
 AAY27444 standard; peptide: 27 AA.
 ID AAY27444
 XX
 AC AAY27444;
 XX
 DT 26-NOV-1999 (first entry)
 XX
 DE Antennapedia internalization sequence in tandem with ezrin fragment.
 XX
 KW Pharmaceutical; curin; mutant; tumor; antennapedia internalization;
 KW metastasis; human.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT Modified-site 22
 FT Modified-site 22
 /note "biotinylated"
 /note "optionally phosphorylated"
 XX
 PN WO947150-A2.
 XX
 PD 23-SEP-1999.
 XX
 PF 18-MAR-1999; 99WO-1PP0254.
 XX
 PR 18-MAR-1998; 98US-0040725.
 XX
 PA (CURI-) INST CURIE.
 PA (CNRS) CNRS CRNT NAT RECH SCI.
 XX
 PI Arpin M, Crepaldi T, Gauthreau A, Louvard D;
 DR WPI: 1999-561851/47.
 XX
 PT New composition for prevention and treatment of tumors and metastasis
 PT
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 Example 5; Page 14; 31pp; English.
 PS
 XX
 The invention provides a pharmaceutical composition containing ezrin
 CC protein, RNA or DNA mutated at tyrosine 353, or a functional fragment
 CC or derivative of the ezrin mutant. The new composition is useful for
 CC prevention and/or treatment of tumors, and especially metastasis. The
 CC treatment sequence represents an autoregulatory internalization sequence in
 CC tandem with an ezrin fragment (residues 448-358). This is used in
 CC experiments of E85 interaction with phosphorylated ezrin peptides.
 XX
 SQ Sequence 27 AA:
 CC
 Query Match 68.3%; Score 41; DB 20; Length 27;

Best Local Similarity 100.0%	Pred. No. 6, 1;	QY	1 EELMRQDYE 11
Matches 8; conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	5 LRLQDYE 12		
XX	1111111111111111		
Db	17 LRLQDYE 24		
RESULT 11		! RESULT 12	
ABG29165	ABB39680 standard; Peptide: 57 AA.	ABB39680 standard; Peptide: 57 AA.	
10 ABG29165 standard; Protein: 344 AA.			
XX		XX	
AC		AC	
ABG29165;	ABB39680;		
XX		XX	
AT 1-FEB-2002 (first entry)		DI 04-FEB-2002 (first entry)	
FE Novel human dienone-ic protein #29165		DE Peptide #7186 derived by human foetal liver single exon probe.	
XX		XX	
FE Human: chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; generic disorder.		KW Human: foetal liver, gene expression, single exon probe, aid probe.	
XX		XX	
KW		KW Human: foetal liver, gene expression, single exon probe, aid probe.	
XX		OS Homo sapiens.	
OS		OS Homo sapiens.	
XX		XX WO200157277-A2.	
PN		PD 09 AUG-2001.	
WO200175047-A2		XX	
PN		PP 30-JAN-2001; 2001WO-US00669.	
11-DEC-2001.		XX	
XX		PR 04-FEB-2000; 2000US-0180412.	
PP 4-MAR-2001; 2001WO-US00669.		PR 25-MAY-2000; 2000US-C207456.	
XX		PR 30-JUN-2000; 2000US-0608408.	
PR 31-MAR-2000; 2000US-0540217.		PR 03-AUG-2000; 2000US-05232366.	
24-AUG-2000; 2000US-0540467.		PR 21-SEP-2000; 2000US-C234687.	
XX		PR 27-SEP-2000; 2000US-0236359.	
PA (HYSER) HYSEQ INN.		PR 04-OCT-2000; 2000US-004263.	
XX		XX	
P1 Darmakar RT, Liu C, Tamq YT;		PA (MOLE-) MOLECULAR DYNAMICS INC.	
XX		XX	
108 WO1 2001-649462/73.		P1 Penn SG, Hanzel DK, Chen W, Rank DR;	
108 N-PSOH: AAS9352.		XX	
XX		DR WPI: 2001-483447/52.	
Now isolated polynucleotides and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.		XX Human genome-derived single exon nucleic acid probes useful for analysing gene expression in human fetal liver.	
PT		XX	
PT New isolated polynucleotides and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.		PS Claim 27; SEQ ID NO 32315; 639pp + sequence listing; English.	
PT		XX	
PT The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences, (I) is useful as hybridisation probes, and as primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (III). The polynucleotides are also used in diagnostics as expressed sequence tags for identification expressed genes. (II) is useful in gene therapy techniques to restore normal activity of (III) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a tool supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG0010 ABG0177 represent novel human diagnostic amino acid sequences of the invention.		CC The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting and displaying gene expression in samples derived from human foetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.	
PT		CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at http://wipo.int/pub/published_pct_sequences .	
PT		XX Sequence 57 AA;	
PS		QY Match 65.0%; Score 49; DB 22; Length 57;	
PS		Best Local Similarity 72.7%; Fred. No. 27;	
PS		Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;	
XX		OT 2 EELMRQDYE 12	
XX		Db 18 ELTRIGEYEE 28	
XX		RESULT 13	
Sequence 344 AA;		ABG0396 standard; Protein: 57 AA.	
QY		XX	
Query Match 68.4%; Score 41; DB 22; Length 44;		AC ABG0396;	
Best Local Similarity 72.7%; Fred. No. 79;		XX	
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;		DT 05 NOV 2001 (first entry)	

PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human placenta -
XX

PS claim 27: SEQ ID NO 33525: 654pp: English.

XX The present invention relates to single exon nucleic acid probes (SENPs; see NAL115 and 15746). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.

XX Sequence 57 AA:

Query Match 65.0%; Score 99; DB 22; Length 57;
Best Local Similarity 72.7%; Precl. No. 27;
Matchers 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 ELMRLQYFE 12
DQ 18 ELMRLQYFE 28

Search completed: January 16, 2003, 16:49:15
Job time: 58.0857 secs